



## SEQUENCE LISTING

RECEIVED

MAY 22 2003

TECH CENTER 1600/2900

&lt;110&gt; Bruce, Wesley B.

<120> A Nitrate-Responsive Root  
Transcriptional Factor

&lt;130&gt; 1263

&lt;140&gt; US 09/970,624

&lt;141&gt; 2001-10-04

&lt;150&gt; US 60/238,292

&lt;151&gt; 2000-10-05

&lt;160&gt; 3

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 1280

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (360)... (1082)

&lt;400&gt; 1

gcacgagccg	ccctgcgcc	agaaaagcca	tcgttcttcc	cacaaacgca	cacatagaag	60
catcattccc	ctctcggcta	gcttcttcc	ctctctccct	cctcctcctc	ttcctcttcc	120
tctctcccttg	ggaaacctgc	tgcttttgag	ctttcttctt	cgagagctcc	caccagatct	180
cctcctcctt	accttctttg	gcacgttcgg	cggcgcgcgc	ggagaaagat	agatcccgcc	240
atcgctgctg	tcggtccttg	cttccgatcg	gagggccaca	accacaacct	ctcgctccat	300
agcgtgcaag	cgcgagccag	ggtcaagaag	agagctagct	agctataggc	cggagatcg	359
atg ggg agg gga	aag atc gtg	atc cgc agg	atc gat aac	tcc acg	agc	407
Met Gly Arg Gly	Lys Ile Val	Ile Arg Arg	Ile Asp Asn	Ser Thr	Ser	
1	5	10	15			

cgg cag gtg acc	ttc tcc aag	cgc cgg aac	ggg atc ttc	aag aag gcc	455
Arg Gln Val Thr	Phe Ser Lys	Arg Arg Asn	Gly Ile Phe	Lys Lys Ala	
20	25	30			

aag gag ctg gcc	atc ctg tgc	gat gcg gag	gtc ggc ctg	gtc atc ttc	503
Lys Glu Leu Ala	Ile Leu Cys	Asp Ala Glu	Val Gly Leu	Val Ile Phe	
35	40	45			

tcc agc acc ggc	cgc ctg tac	gag tac tct	agc acc agc	atg aaa tca	551
Ser Ser Thr Gly	Arg Leu Tyr	Glu Tyr Ser	Ser Thr Ser	Met Lys Ser	
50	55	60			

gtt ata gat cgg	tac ggc aag	gcc aag gaa	gag cag caa	gtc gtc gca	599
Val Ile Asp Arg	Tyr Gly Lys	Ala Lys Glu	Glu Gln Gln	Val Val Ala	
65	70	75	80		

aat ccc aac tcg	gag ctt aag	ttt tgg caa	agg gag gca	gca agc ttg	647
Asn Pro Asn Ser	Glu Leu Lys	Phe Trp Gln	Arg Glu Ala	Ala Ser Leu	

85	90	95	
aga caa caa ctg cac aac ttg caa gaa aat tat cgg cag ttg acg gga			695
Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly			
100	105	110	
gat gat ctt tct ggg ctg aat gtc aaa gaa ctg cag tcc ctg gag aat			743
Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn			
115	120	125	
caa ttg gaa aca agc ctg cgt ggt gtc cgc gca aag aag gac cat ctc			791
Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu			
130	135	140	
ttg ata gat gag att cac gat ttg aat cga aag gca agt tta ttt cac			839
Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His			
145	150	155	160
caa gaa aat aca gac ttg tac aat aag atc aac ctg att cgc caa gaa			887
Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu			
165	170	175	
aat gat gag tta cat aaa aag ata tat gag act gaa gga cca agt gga			935
Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly			
180	185	190	
gtt aat cgg gag tca ccg act cca ttc aac ttt gca gta gta gaa acc			983
Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr			
195	200	205	
aga gat gtt cct gtg caa ctt gaa ctc agc aca ctg cca cag caa aat			1031
Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn			
210	215	220	
aac att gag cca tct act gct cct aag cta gga ttg caa tta att cca			1079
Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro			
225	230	235	240
tga agaagagtaa aactgccgtc ttatgatgct gaaggaaact atttattgtg			1132
*			
aagagatgat actcagagaa agacatattt gtggcagggg gatttgagat atgaacttat			1192
aaatgtaatg caaataattt tcagaccgga atggggctcgt ggaattcaga ggatgattgc			1252
tttctaaaaa aaaaaaaaaa aaaaaaaa			1280
<210> 2			
<211> 240			
<212> PRT			
<213> Zea mays			
<400> 2			
Met Gly Arg Gly Lys Ile Val Ile Arg Arg Ile Asp Asn Ser Thr Ser			
1 5 10 15			
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala			
20 25 30			
Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe			
35 40 45			

Ser	Ser	Thr	Gly	Arg	Leu	Tyr	Glu	Tyr	Ser	Ser	Thr	Ser	Met	Lys	Ser
50						55					60				
Val	Ile	Asp	Arg	Tyr	Gly	Lys	Ala	Lys	Glu	Glu	Gln	Gln	Val	Val	Ala
65					70				75						80
Asn	Pro	Asn	Ser	Glu	Leu	Lys	Phe	Trp	Gln	Arg	Glu	Ala	Ala	Ser	Leu
				85					90					95	
Arg	Gln	Gln	Leu	His	Asn	Leu	Gln	Glu	Asn	Tyr	Arg	Gln	Leu	Thr	Gly
			100					105					110		
Asp	Asp	Leu	Ser	Gly	Leu	Asn	Val	Lys	Glu	Leu	Gln	Ser	Leu	Glu	Asn
		115					120					125			
Gln	Leu	Glu	Thr	Ser	Leu	Arg	Gly	Val	Arg	Ala	Lys	Lys	Asp	His	Leu
		130				135					140				
Leu	Ile	Asp	Glu	Ile	His	Asp	Leu	Asn	Arg	Lys	Ala	Ser	Leu	Phe	His
145					150					155					160
Gln	Glu	Asn	Thr	Asp	Leu	Tyr	Asn	Lys	Ile	Asn	Leu	Ile	Arg	Gln	Glu
				165					170					175	
Asn	Asp	Glu	Leu	His	Lys	Lys	Ile	Tyr	Glu	Thr	Glu	Gly	Pro	Ser	Gly
			180					185					190		
Val	Asn	Arg	Glu	Ser	Pro	Thr	Pro	Phe	Asn	Phe	Ala	Val	Val	Glu	Thr
		195					200					205			
Arg	Asp	Val	Pro	Val	Gln	Leu	Glu	Leu	Ser	Thr	Leu	Pro	Gln	Gln	Asn
		210				215					220				
Asn	Ile	Glu	Pro	Ser	Thr	Ala	Pro	Lys	Leu	Gly	Leu	Gln	Leu	Ile	Pro
225					230					235					240

<210> 3  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<400> 3  
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36